REMARKS

After entry of this amendment, claims 1-3, 6-17, 19-20 and 22-25 are pending, of which claims 12 and 13 are withdrawn. Claims 4, 5, 18 and 21 have been cancelled without prejudice or disclaimer, and the subject matter of claims 5 and 21 has been incorporated into claims 1 and 14 as amended. New claims 22-25 have been added. The claims have been amended without prejudice or disclaimer to better comply with U.S. practice, to delete the non-elected subject matter, to correct the antecedent basis, and to address the various points made in the Official Action. The amended claims find support *inter alia* in the original claims. Further support for the amended claim 1 and the added claims 22-23 is found in the original claim 5 and in the specification at page 55, lines 39-43. Claim 1 finds additional support throughout the specification, for instance, at page 73, lines 4-6 for the recitation of "by transformation," and at page 36, lines 35-41 for the recitation of stress factors. Further support for the amended claim 14 and the added claims 24-25 is found in the original claims 5 and 21 and in the specification at page 55, lines 39-43. Further support for the amended claim 17 is found in the original claim 18. No new matter has been added.

Sequence Listing

The Examiner requires that the sequence at page 49, lines 13-14, be identified by sequence identifying number. However, Applicants are unable to identify any sequences at page 49. Thus, clarification is respectfully requested.

The Examiner further requires that the sequences in Figures 1 and 6 be identified by sequence identifying number. In response, the sequences in Figures 1 and 6 not appearing in the Sequence Listing has been added to the Sequence Listing attached hereto in compact disc. The corresponding sequence identifying numbers have also been added to the brief description of the drawings in the specification to comply with 37 CFR § 1.821(a) and (d). No new matter has been added.

Applicants submit herewith replacement copies of the Sequence Listing (COPY 1 and COPY 2) that conform to 37 CFR §§ 1.821-1.825 and the Sequence Listing in computer readable form, all on compact disc, accompanied by a Statement to Support Filing and Submission in Accordance with 37 CFR §§ 1.821-1.825. The specification has also been amended to insert the required paragraph for submission of Sequence Listing only on compact disc. No new matter

has been added to the Sequence Listing or the specification. Entry of this Sequence Listing into the application is respectfully requested.

Specification

In the specification at pages 1 and 4, appropriate section headings have been added as suggested by the Examiner. Additionally, a section entitled "BRIEF DESCRIPTION OF THE DRAWINGS" has been inserted at page 4 to accommodate the figure legends found at pages 77-80. Support is found *inter alia* in the specification at pages 77-80 and can be summarize in the following table:

Figure No.	Support found in the specification at:	
	Page No(s).	Line No(s).
1	77	6-17
2	77	19-23
3	77	25-29
4	77	31-35
5	77	37-41
6	77-78	43-44, 1-7
7	78	9-21
8	78	23-30
9	78-79	32-44, 1-8
10	79	10-27
11	79	29-39
12	79-80	41-43, 1-7
13	80	9-12

Additionally, page 38 of the specification has been amended to delete the hyperlink. It is noted that the information referenced in the hyperlink is available in the art and is referenced in the articles cited in the specification. No new matter has been added.

It is further noted that the Examiner also requires the deletion of hyperlink contained at page 49, line 29. However, Applicants are unable to identify any hyperlink at page 49. Thus, it is believed that this objection is moot.

Claim Objections

In view of the present amendment, it is believed that the claim objections are rendered moot.

Rejections under 35 U.S.C. § 112, second paragraph

Claim 11 is rejected under 35 U.S.C. § 112, second paragraph, for indefiniteness. The Examiner argues that the claim is unclear as to the source of the "MLO," "RacB," "NaOx," "PEN2," "SNAP34," and "PEN1."

Applicants disagree and respectfully submit that one skilled in the art would recognize on the face of the claim language that the inhibited or reduced expression or function of "MLO," "RacB," and "NaOx" can result from either mutation or transgene expression. Furthermore, as described in the specification, the processes or methods for reducing or inhibiting the activity or function of "MLO," "RacB," and "NaOx" are known in the art. See Specification at pages 11-13. For example, WO 98/04586, WO 99/47552, and WO 00/01722 disclose the Mlo locus and the method of inhibiting or reducing the activity or function of MLO. See Specification at pages 11-12. The equivalent teaching for RacB and NaOx can also be found in WO 2003/020939 and PCT/EP03/07589, respectively. See Specification at pages 12-13. As taught in these references, which are expressly incorporated by reference in the present application, the inhibited or reduced expression or function of these genes may be achieved by way of mutagenesis or by way of transgenic overexpression.

Similarly, one skilled in the art would also recognize that the increased expression or function of "PEN2," "SNAP34," and "PEN1" can result from either mutation or transgene expression. As described in WO 03/074688, the content of which is also expressly incorporated by reference into the specification, the activity or function of "PEN2" may be increased by way of mutagenesis or transgenic overexpression. Likewise, the activity or function of "SNAP34" and "PEN1" can be increased analogously using the methods described in WO 03/074688 with the "SNAP34" and "PEN1" sequences disclosed in the present application or otherwise known in the art. Thus, it is clear to one skilled in the art that the source of the increased expression or function of these genes may be by mutation or by transgene expression.

Reconsideration and withdrawal of this rejection is respectfully requested.

The Examiner further finds claims 11 and 20 indefinite for reciting "mlo-resistant phenotype," alleging that the term is not defined in the specification and such wording is open to various interpretations leading to indefiniteness. Applicants respectfully traverse.

As discussed above, the Mlo locus is known in the art. Furthermore, the "mlo-resistant phenotype" is well characterized in the art. For instance, WO 98/04586 describes that the "mlo-

resistant phenotype" could exhibit a leaf lesion phenotype and confers an apparently durable, broad spectrum resistance to the powdery mildew pathogen, *Erysiphe graminis* f sp *hordei*. See WO 98/04586, page 1, lines 19-22. Similarly, WO 99/47552 described that the "mlo-resistant phenotype" in the cellular level involves the formation of large cell wall appositions, called papillae, at the contact sites with the pathogen. Such cell wall appositions prevent the penetration of the pathogen, thus providing resistance. See WO 99/47552, paragraph bridging pages 1-2. Thus, it is clear that the term "mlo-resistant phenotype" is well defined in the art and a skilled artisan would recognize such a phenotype regardless of the source of such a resistance.

Reconsideration and withdrawal of the rejection is respectfully requested.

Claims 15 and 21 are rejected for lack of antecedent basis. In view of the present amendment, the rejection is rendered moot.

Rejections under 35 U.S.C. § 112, first paragraph

Claims 1-11 and 14-21 are rejected under 35 U.S.C. § 112, first paragraph, for allegedly lacking an enabling disclosure and failing to comply with the written description requirement. Applicants respectfully disagree and traverse the rejections in view of the present amendments.

Enablement Rejection

The Examiner rejects the claims for lack of enablement, alleging that the specification is not enabling for methods of increasing amount or function of a BI1 protein in a plant other than by transformation. The Examiner further asserts that the specification is not enabling for methods that use sequences as recited in the claims. Additionally, the Examiner alleges that the claims are not enabled for increasing resistance to all biotic and abiotic stresses using BI1 protein or variants thereof. Applicants respectfully disagree. However, to expedite prosecution, the claims have been amended without prejudice and disclaimer to recite the BI1 protein as defined, not broadly, as sequences having at least 70% identity with the sequence of SEQ ID NO: 2. Furthermore, the claim requires that the increase of BI1 protein amount or function is due to transformation, thereby adopting the Examiner's suggestion in this respect. Additionally, the claims further recite the biotic or abiotic stress factors which are improved by the claimed method. It is noted however that, the improved resistance achieved by the claimed method may

also improve resistance to other unidentified stress factors. It is therefore submitted that the more commensurate scope of the claims as amended overcomes the rejection.

The Examiner further argues that screening for substitutions or modifications is not routine and results of modifications are unpredictable. The Examiner also asserts that the state of the art is unpredictable. Applicants respectfully disagree.

It is respectfully submitted that the more commensurate scope of the claims as amended overcomes these concerns. Furthermore, as described in the specification, BI1 is a highly conserved protein. Motifs which are conserved between various BI1 proteins of different origins can be identified easily by sequence alignment as demonstrated in Figures 1 and 6. Thus, when preparing a BI1 protein for the use of the claimed method, one skilled in the art would find guidance as modifying, substituting or deleting amino acid residues. From this guidance, a person skilled in the art would investigate mutations least likely to impair function. Methods of generating such mutations, for example, site-direct mutagenesis and PCT-mediated mutagenesis, are standard techniques readily available and known to those skilled in the art. Screening such mutants for activity would be readily within the skill of the art. The need for routine experimentation does not defeat enablement, since it is the quality and not the quantity of necessary experimentation which is relevant.

In view of the detailed description, guidance, working examples, and high level of skill, the specification enables the full scope of the claims as amended without undue experimentation. On these facts, an analysis under *In re Wands* supports enablement. *In re Wands*, 858 F.2d 731, 737 (Fed. Cir. 1988) (routine screening of hybridomas was not "undue experimentation;" the involved experimentation can be considerable, so long as "routine").

For these reasons and in light of the amendments, reconsideration and withdrawal of this rejection is respectfully requested.

Written Description Rejection

The Examiner alleges that the specification does not provide an adequate written description for the claimed genus of sequences. To address this concern, Applicants have amended the claims without prejudice or disclaimer to recite the BI1 protein with more specificity based, in the broadest aspect, on percent identity to the recited SEQ ID NO: 2. For

example, claim 1 has been amended to recite the BI1 protein based on the polypeptide sequence of SEQ ID NO: 2, and variants having at least 70% identity to SEQ ID NO: 2.

Furthermore, it is respectfully submitted that the specification provides a representative number of species within the claimed genus. This is a proper means of complying with the written description requirement. As stated in *Eli Lilly and Co.*, "[a] description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs." 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). As described in the specification and shown in Figure 1, the numerous BI1 proteins from various plant species share a high degree of sequence identity with the sequence of SEQ ID NO: 2. Amongst these sequences, SEQ ID NOs: 8 (88% identity to SEQ ID NO: 2), 18 (83% identity to SEQ ID NO: 2), 20 (97% identity to SEQ ID NO: 2), 22 (85% identity to SEQ ID NO: 2), 24 (81% identity to SEQ ID NO: 2), 28 (71% identity to SEQ ID NO: 2), and 68 (88% identity to SEQ ID NO: 2) show more than 70% identity with SEQ ID NO: 2, according to the sequence alignment using ClustalW (available at http://www.ebi.ac.uk/Tools/clustalw/index.html).

Because these seven sequences clearly constitute a representative number of species within the genus recited in the amended claims, it is respectfully submitted that the claims as amended satisfy the written description requirement.

Reconsideration and withdrawal of the rejection is respectfully requested.

Rejections under 35 U.S.C. § 102

Claims 14 and 16-20 are rejected as being anticipated under § 102(b) by Flinn et al. ("Flinn"). Claims 16-20 are further rejected as being anticipated under § 102(e) by Reed ("Reed").

Flinn discloses plant BI1 proteins (SEQ ID NOs: 87 and 88 of Flinn) which share less than 70% identity with the sequence of SEQ ID NO: 2, according to the sequence comparison using ClustalW.

Similarly, Reed discloses a tomato BI1 protein (SEQ ID NO: 4 of Reed) which shares less than 70% identity with the sequence of SEQ ID NO: 2, according to the sequence comparison using ClustalW.

It is submitted that in view of the present amendment, the references cited by the Examiner do not anticipate the claims. Reconsideration and withdrawal of this rejection is respectfully requested.

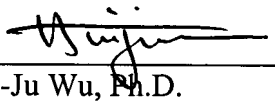
CONCLUSION

For at least the above reasons, Applicants respectfully request withdrawal of the rejections and allowance of the claims.

Applicants reserve all rights to pursue the non-elected claims and subject matter in one or more divisional applications.

Accompanying this response is a petition for a three-month extension of time to and including November 1, 2007, to respond to the Office Action mailed May 1, 2007 with the required fee authorization, including the fee for extra claims. No further fees are believed due. If any additional fee is due, please charge our Deposit Account No. 03-2775, under Order No. 12810-00137-US from which the undersigned is authorized to draw

Respectfully submitted,

By 

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